

## SEQUENCE LISTING

<110> Jaworski, Jan G.  
Blacklock, Brenda J.

<120> FATTY ACID ELONGASE 3-KETOACYL COA  
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<151> 2001-06-08

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Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn	
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 35 40 45  
 Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val  
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Leu Leu Ala Phe Thr Val Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg	
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Pro Lys Pro Val Tyr Leu Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr	
75 80 85	
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Arg Lys Ala Asp Pro Ser Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp	
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125 130 135	
acc cac ggg ccc gag ggg ctg ctt cag gtc cct ccc cgg aag act ttt	543
Thr His Gly Pro Glu Gly Leu Leu Gln Val Pro Pro Arg Lys Thr Phe	
140 145 150	
gcg cgc gcg cgt gaa gag acg gag caa gtt atc att ggt gcg cta gaa	591
Ala Arg Ala Arg Glu Glu Thr Glu Gln Val Ile Ile Gly Ala Leu Glu	
155 160 165	
aat cta ttc aag aac acc aat gtt aac cct aaa gat ata ggt ata ctt	639
Asn Leu Phe Lys Asn Thr Asn Val Asn Pro Lys Asp Ile Gly Ile Leu	
170 175 180 185	
gtg gtg aac tca agc atg ttt aat cca act cct tgc ctc tcc gcg atg	687

Val	Val	Asn	Ser	Ser	Met	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	
				190					195					200		
gtc	gtt	aac	act	ttc	aag	ctc	cga	agc	aac	gta	aga	agc	ttt	aac	ctt	735
Val	Val	Asn	Thr	Phe	Lys	Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	
			205					210					215			
ggc	ggc	atg	ggc	tgt	agt	gcc	ggc	gtt	ata	gcc	att	gat	cta	gca	aag	783
Gly	Gly	Met	Gly	Cys	Ser	Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	
		220					225					230				
gac	ttg	ttg	cat	gtc	cat	aaa	aat	acg	tat	gct	ctt	gtg	gtg	agc	aca	831
Asp	Leu	Leu	His	Val	His	Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	
	235					240					245					
gag	aac	atc	act	tat	aac	att	tac	gct	ggc	gat	aat	agg	tcc	atg	atg	879
Glu	Asn	Ile	Thr	Tyr	Asn	Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	
250					255				260					265		
gtt	tca	aat	tgc	ttg	ttc	cgt	gtt	ggc	ggg	gcc	gct	att	ttg	ctc	tcc	927
Val	Ser	Asn	Cys	Leu	Phe	Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	
				270				275						280		
aac	aag	cct	aga	gat	cgt	aga	cgg	tcc	aag	tac	gag	cta	gtt	cac	acg	975
Asn	Lys	Pro	Arg	Asp	Arg	Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	
			285					290					295			
gtt	cga	acg	cat	acc	gga	gct	gac	gac	aag	tct	ttt	cgt	tgc	gtg	caa	1023
Val	Arg	Thr	His	Thr	Gly	Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	
		300					305					310				
caa	gga	gac	gat	gag	aac	ggc	caa	acc	gga	gtg	agt	ttg	tcc	aag	gac	1071
Gln	Gly	Asp	Asp	Glu	Asn	Gly	Gln	Thr	Gly	Val	Ser	Leu	Ser	Lys	Asp	
	315					320					325					
ata	acc	gat	gtt	gct	ggc	cga	acg	gtt	aag	aaa	aac	ata	gca	acg	ctg	1119
Ile	Thr	Asp	Val	Ala	Gly	Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	
330				335					340					345		
ggc	ccg	ttg	att	ctt	ccg	tta	agc	gag	aaa	ctt	ctt	ttt	ttc	gtt	acc	1167
Gly	Pro	Leu	Ile	Leu	Pro	Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	
				350					355					360		
ttc	atg	ggc	aag	aaa	ctt	ttc	aaa	gac	gaa	atc	aaa	cat	tat	tac	gtc	1215
Phe	Met	Gly	Lys	Lys	Leu	Phe	Lys	Asp	Glu	Ile	Lys	His	Tyr	Tyr	Val	
			365					370					375			
ccg	gac	ttc	aag	ctt	gct	atc	gac	cat	ttt	tgt	ata	cat	gcc	gga	ggc	1263
Pro	Asp	Phe	Lys	Leu	Ala	Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	
		380					385					390				
aaa	gcc	gtg	att	gat	gtg	cta	gag	aag	aac	cta	ggc	cta	gca	ccg	atc	1311
Lys	Ala	Val	Ile	Asp	Val	Leu	Glu	Lys	Asn	Leu	Gly	Leu	Ala	Pro	Ile	
	395					400					405					
gat	gta	gag	gca	tca	aga	tca	acg	tta	cat	aga	ttt	gga	aac	act	tca	1359

Asp Val Glu Ala Ser Arg Ser Thr Leu His Arg Phe Gly Asn Thr Ser  
 410 415 420 425  
 tct agc tca ata tgg tat gag ttg gca tac ata gaa ccc aaa gga agg 1407  
 Ser Ser Ser Ile Trp Tyr Glu Leu Ala Tyr Ile Glu Pro Lys Gly Arg  
 430 435 440  
 atg aag aaa ggt aat aaa gtt tgg cag att gct tta ggg tca ggc ttt 1455  
 Met Lys Lys Gly Asn Lys Val Trp Gln Ile Ala Leu Gly Ser Gly Phe  
 445 450 455  
 aag tgt aac agt gca gtt tgg gtg gct cta aac aat gtc aaa gct tca 1503  
 Lys Cys Asn Ser Ala Val Trp Val Ala Leu Asn Asn Val Lys Ala Ser  
 460 465 470  
 aca aat agt cct tgg gaa cac tgc atc gac aga tac ccg gtt aaa att 1551  
 Thr Asn Ser Pro Trp Glu His Cys Ile Asp Arg Tyr Pro Val Lys Ile  
 475 480 485  
 gat tct gat tca ggt aag tca gag act cgt gtc cca aac ggt cgg tcc 1599  
 Asp Ser Asp Ser Gly Lys Ser Glu Thr Arg Val Pro Asn Gly Arg Ser  
 490 495 500 505  
 taataaatga tgtttgctct ctttcgtttc tttttattgg ttataataat ttgatggcca 1659  
 cgatgtttct cttgtttgtt atgaataaag aatcccacgg tgttctagta aaaaaaaaaa 1719  
 aaaaaaaaaa aaaaaaa 1736

&lt;210&gt; 6

&lt;211&gt; 505

&lt;212&gt; PRT

&lt;213&gt; Brassica napus

&lt;400&gt; 6

Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn  
 1 5 10 15  
 Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys  
 20 25 30  
 Ala Tyr Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr Leu  
 35 40 45  
 Gln His Asn Leu Ile Thr Ile Ala Pro Leu Leu Ala Phe Thr Val Phe  
 50 55 60  
 Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu Val  
 65 70 75 80  
 Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile Ser  
 85 90 95  
 Lys Val Met Asp Ile Phe Phe Gln Val Arg Lys Ala Asp Pro Ser Arg  
 100 105 110  
 Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys Ile  
 115 120 125  
 Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly Leu  
 130 135 140  
 Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Arg Ala Arg Glu Glu Thr  
 145 150 155 160  
 Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr Asn  
 165 170 175  
 Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met Phe

			180					185					190			
Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	Leu	
		195					200					205				
Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	Ala	
	210					215					220					
Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	Lys	
225					230					235					240	
Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	Ile	
				245					250					255		
Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	Arg	
			260					265					270			
Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Arg	Asp	Arg	Arg	
		275					280					285				
Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	Ala	
	290					295					300					
Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn	Gly	
305					310					315					320	
Gln	Thr	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly	Arg	
				325				330						335		
Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro	Leu	
			340					345					350			
Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu	Phe	
		355					360					365				
Lys	Asp	Glu	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala	Ile	
	370					375					380					
Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Lys	Ala	Val	Ile	Asp	Val	Leu	
385					390					395					400	
Glu	Lys	Asn	Leu	Gly	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg	Ser	
				405					410					415		
Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr	Glu	
			420					425					430			
Leu	Ala	Tyr	Ile	Glu	Pro	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys	Val	
		435					440					445				
Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val	Trp	
	450					455					460					
Val	Ala	Leu	Asn	Asn	Val	Lys	Ala	Ser	Thr	Asn	Ser	Pro	Trp	Glu	His	
465					470					475					480	
Cys	Ile	Asp	Arg	Tyr	Pro	Val	Lys	Ile	Asp	Ser	Asp	Ser	Gly	Lys	Ser	
				485					490					495		
Glu	Thr	Arg	Val	Pro	Asn	Gly	Arg	Ser								
			500					505								

<210> 7

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 342 bp from *A. thaliana* FAE1 (SEQ ID NO:1) and  
3' 1179 bp from *B. napus* elongase KCS (SEQ ID  
NO:3); designated At114

<221> CDS

<222> (1) ... (1518)

<400> 7

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1 5 10 15	
ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa	96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	
ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	
gac tac tcg tgt tac ctt ccg cca ccg cat ctc aaa gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser	
85 90 95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	
cgg aac ggc acg tgt gat gat tcg tcg tgg ctt gac ttc ttg agg aag	384
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly	
130 135 140	
ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag	480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu	
145 150 155 160	
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc	528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	
165 170 175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg	576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt	672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	

gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat	720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	
245 250 255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc	816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt	864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg	
275 280 285	
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga	912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly	
290 295 300	
gct gac ggc aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac	960
Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn	
305 310 315 320	
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt	1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly	
325 330 335	
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg	1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	
340 345 350	
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt	1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu	
355 360 365	
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct	1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	
370 375 380	
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg	1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val	
385 390 395 400	
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga	1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg	
405 410 415	
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat	1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr	
420 425 430	
gag ttg gca tac ata gaa rca aaa gga agg atg aag aaa ggt aat aaa	1344
Glu Leu Ala Tyr Ile Glu Xaa Lys Gly Arg Met Lys Lys Gly Asn Lys	
435 440 445	

gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt 1392  
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val  
 450 455 460

tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa 1440  
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu  
 465 470 475 480

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag 1488  
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys  
 485 490 495

tca gag act cgt gtc cca aac ggt cgg tcc taa 1521  
 Ser Glu Thr Arg Val Pro Asn Gly Arg Ser  
 500 505

<210> 8

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<221> VARIANT

<222> (0)...(0)

<223> Xaa = Ala or Thr

<223> 5' 114 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 392 amino acids from B. napus elongase KCS (SEQ ID NO:4); designated At114

<400> 8

Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn  
 1 5 10 15  
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys  
 20 25 30  
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu  
 35 40 45  
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe  
 50 55 60  
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val  
 65 70 75 80  
 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser  
 85 90 95  
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser  
 100 105 110  
 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys  
 115 120 125  
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly  
 130 135 140  
 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu  
 145 150 155 160  
 Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr  
 165 170 175  
 Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met  
 180 185 190

Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys  
           195                          200                          205  
 Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser  
           210                          215                          220  
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His  
 225                          230                          235                          240  
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn  
                           245                          250                          255  
 Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe  
                           260                          265                          270  
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg  
                           275                          280                          285  
 Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly  
           290                          295                          300  
 Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn  
 305                          310                          315                          320  
 Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly  
                           325                          330                          335  
 Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro  
                           340                          345                          350  
 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu  
           355                          360                          365  
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala  
           370                          375                          380  
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val  
 385                          390                          395                          400  
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg  
                           405                          410                          415  
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr  
                           420                          425                          430  
 Glu Leu Ala Tyr Ile Glu Xaa Lys Gly Arg Met Lys Lys Gly Asn Lys  
           435                          440                          445  
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val  
           450                          455                          460  
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu  
 465                          470                          475                          480  
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys  
                           485                          490                          495  
 Ser Glu Thr Arg Val Pro Asn Gly Arg Ser  
                           500                          505

<210> 9

<211> 1518

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 222 bp from A. thaliana FAE1 (SEQ ID NO:1) and  
 3' 1296 bp from B. napus elongase KCS (SEQ ID  
 NO:3); designated At74

<221> CDS

<222> (1)...(1515)

<400> 9

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Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn	
1				5					10					15		
ttt	ttc	aac	ctc	tgt	ttg	ttc	ccg	tta	acg	gcg	ttc	ctc	gcc	gga	aaa	96
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys	
			20					25					30			
gcc	tct	cgg	ctt	acc	ata	aac	gat	ctc	cac	aac	ttc	ctt	tcc	tat	ctc	144
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu	
			35				40					45				
caa	cac	aac	ctt	ata	aca	gta	act	tta	ctc	ttt	gct	ttc	act	ggt	ttc	192
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe	
	50					55				60						
ggt	ttg	ggt	ctc	tac	atc	gta	acc	cga	ccc	aaa	ccg	ggt	tac	ctc	ggt	240
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Lys	Pro	Val	Tyr	Leu	Val	
65					70					75					80	
gag	tac	tca	tgc	tac	ctt	cca	cca	acg	cat	tgt	aga	tca	agt	atc	tcc	288
Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	His	Cys	Arg	Ser	Ser	Ile	Ser	
				85					90					95		
aag	gtc	atg	gat	atc	ttt	tat	caa	gta	aga	aaa	gct	gat	cct	tct	cgg	336
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	Pro	Ser	Arg	
			100					105					110			
aac	ggc	acg	tgc	gat	gac	tcg	tcg	tgg	ctt	gac	ttc	ttg	agg	aag	att	384
Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys	Ile	
			115				120					125				
caa	gaa	cgt	tca	ggt	cta	ggc	gat	gaa	act	cac	ggg	ccc	gag	ggg	ctg	432
Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly	Leu	
	130					135					140					
ctt	cag	gtc	cct	ccc	cgg	aag	act	ttt	gcg	gcg	gcg	cgt	gaa	gag	acg	480
Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu	Thr	
145					150				155						160	
gag	caa	ggt	atc	att	ggt	gcg	cta	gaa	aat	cta	ttc	aag	aac	acc	aac	528
Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr	Asn	
				165					170					175		
ggt	aac	cct	aaa	gat	ata	ggt	ata	ctt	gtg	gtg	aac	tca	agc	atg	ttt	576
Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	Phe	
			180					185					190			
aat	cca	act	cca	tcg	ctc	tcc	gcg	atg	gtc	ggt	aac	act	ttc	aag	ctc	624
Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	Leu	
			195				200					205				
cga	agc	aac	gta	aga	agc	ttt	aac	ctt	ggt	ggc	atg	ggt	tgt	agt	gcc	672
Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	Ala	
	210					215					220					
ggc	ggt	ata	gcc	att	gat	cta	gca	aag	gac	ttg	ttg	cat	gtc	cat	aaa	720

Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	Lys	
225					230					235					240	
aat	acg	tat	gct	ctt	gtg	gtg	agc	aca	gag	aac	atc	act	tat	aac	att	768
Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	Ile	
				245					250					255		
tac	gct	ggg	gat	aat	agg	tcc	atg	atg	gtt	tca	aat	tgc	ttg	ttc	cgt	816
Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	Arg	
			260					265					270			
gtt	ggg	ggg	gcc	gct	att	ttg	ctc	tcc	aac	aag	cct	gga	gat	cgt	aga	864
Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	Arg	
		275					280					285				
cgg	tcc	aag	tac	gag	cta	gtt	cac	acg	gtt	cga	acg	cat	acc	gga	gct	912
Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	Ala	
	290					295				300						
gac	ggc	aag	tct	ttt	cgt	tgc	gtg	caa	caa	gga	gac	gat	gag	aac	ggc	960
Asp	Gly	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn	Gly	
305				310						315				320		
aaa	atc	gga	gtg	agt	ttg	tcc	aag	gac	ata	acc	gat	gtt	gct	ggg	cga	1008
Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly	Arg	
				325				330					335			
acg	gtt	aag	aaa	aac	ata	gca	acg	ttg	ggg	ccg	ttg	att	ctt	ccg	tta	1056
Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro	Leu	
			340					345					350			
agc	gag	aaa	ctt	ctt	ttt	ttc	gtt	acc	ttc	atg	ggc	aag	aaa	ctt	ttc	1104
Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu	Phe	
		355					360				365					
aaa	gat	aaa	atc	aaa	cat	tac	tac	gtc	ccg	gat	ttc	aaa	ctt	gct	att	1152
Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala	Ile	
	370					375				380						
gac	cat	ttt	tgt	ata	cat	gcc	gga	ggc	aga	gcc	gtg	att	gat	gtg	cta	1200
Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val	Leu	
385					390					395					400	
gag	aag	aac	cta	gcc	cta	gca	ccg	atc	gat	gta	gag	gca	tca	aga	tca	1248
Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg	Ser	
				405					410				415			
acg	tta	cat	aga	ttt	gga	aac	act	tca	tct	agc	tca	ata	tgg	tat	gag	1296
Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr	Glu	
			420					425					430			
ttg	gca	tac	ata	gaa	gca	aaa	gga	agg	atg	aag	aaa	ggg	aat	aaa	gtt	1344
Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys	Val	
		435					440					445				
tgg	cag	att	gct	tta	ggg	tca	ggc	ttt	aag	tgt	aac	agt	gca	gtt	tgg	1392

Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp  
 450 455 460  
 gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa cac 1440  
 Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu His  
 465 470 475 480  
 tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag tca 1488  
 Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys Ser  
 485 490 495  
 gag act cgt gtc caa aac ggt cgg tcc taa 1518  
 Glu Thr Arg Val Gln Asn Gly Arg Ser  
 500 505

<210> 10  
 <211> 505  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> 5' 74 amino acids from *A. thaliana* FAE1 (SEQ ID NO:2) and 3' 431 amino acids from *B. napus* elongase KCS (SEQ ID NO:4); designated At74

<400> 10  
 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn  
 1 5 10 15  
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys  
 20 25 30  
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu  
 35 40 45  
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe  
 50 55 60  
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Lys Pro Val Tyr Leu Val  
 65 70 75 80  
 Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile Ser  
 85 90 95  
 Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser Arg  
 100 105 110  
 Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys Ile  
 115 120 125  
 Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly Leu  
 130 135 140  
 Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu Thr  
 145 150 155 160  
 Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr Asn  
 165 170 175  
 Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met Phe  
 180 185 190  
 Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys Leu  
 195 200 205  
 Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser Ala  
 210 215 220  
 Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His Lys

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225          230          235          240
Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn Ile
          245          250          255
Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe Arg
          260          265          270
Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg Arg
          275          280          285
Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly Ala
          290          295          300
Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn Gly
305          310          315          320
Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly Arg
          325          330          335
Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro Leu
          340          345          350
Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu Phe
          355          360          365
Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala Ile
          370          375          380
Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val Leu
385          390          395          400
Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg Ser
          405          410          415
Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr Glu
          420          425          430
Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys Val
          435          440          445
Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp
          450          455          460
Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu His
465          470          475          480
Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys Ser
          485          490          495
Glu Thr Arg Val Gln Asn Gly Arg Ser
          500          505

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<210> 11

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and  
3' 1179 bp from B. napus elongase KCS (SEQ ID  
NO:3) having mutations at positions 271, 272 and  
275; designated At114 L91C K92R

<221> CDS

<222> (1)...(1518)

<400> 11

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atg acg tcc gtt aac gtt aag ctc ctt tac cgt tat gtc tta acc aac      48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
  1              5              10              15

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ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa      96

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Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys	
		20						25					30			
gcc	tct	cgg	ctt	acc	ata	aac	gat	ctc	cac	aac	ttc	ctt	tcc	tat	ctc	144
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu	
		35					40					45				
caa	cac	aac	ctt	ata	aca	gta	act	tta	ctc	ttt	gct	ttc	act	gtt	ttc	192
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe	
		50				55					60					
ggg	ttg	gtt	ctc	tac	atc	gta	acc	cga	ccc	aac	ccg	gtt	tat	ctc	gtt	240
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val	
	65				70					75					80	
gac	tac	tcg	tgt	tac	ctt	ccg	cca	ccg	cat	tgc	aga	gtt	agt	gtc	tct	288
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Cys	Arg	Val	Ser	Val	Ser	
			85						90					95		
aaa	gtc	atg	gat	att	ttc	tac	caa	ata	aga	aaa	gct	gat	act	tct	tca	336
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser	
			100					105					110			
cgg	aac	ggc	acg	tgt	gat	aac	tcg	tcg	tgg	ctt	gac	ttc	ttg	agg	aag	384
Arg	Asn	Gly	Thr	Cys	Asp	Asn	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys	
		115					120					125				
att	caa	gaa	cgt	tca	ggg	cta	ggc	gat	gaa	act	cac	ggg	ccc	gag	ggg	432
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly	
	130					135					140					
ctg	ctt	cag	gtc	cct	ccc	cgg	aag	act	ttt	gcg	gcg	gcg	cgt	gaa	gag	480
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu	
	145				150					155					160	
acg	gag	caa	gtt	atc	att	ggg	gcg	cta	gaa	aac	cta	ttc	aag	aac	acc	528
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr	
				165				170						175		
aac	gtt	aac	cct	aaa	gat	ata	ggg	ata	ctt	gtg	gtg	aac	tca	agc	atg	576
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	
			180					185					190			
ttt	aac	cca	act	cca	tcg	ctc	tcc	gcg	atg	gtc	gtt	aac	act	ttc	aag	624
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	
		195					200					205				
ctc	cga	agc	aac	gta	aga	agc	ttt	aac	ctt	ggg	ggc	atg	ggg	tgt	agt	672
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	
	210					215					220					
gcc	ggc	gtt	ata	gcc	att	gat	cta	gca	aag	gac	ttg	ttg	cat	gtc	cat	720
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	
	225				230					235					240	
aaa	aac	acg	tat	gct	ctt	gtg	gtg	agc	aca	gag	aac	atc	act	tat	aac	768

Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	
				245					250					255		
att	tac	gct	ggg	gat	aat	agg	tcc	atg	atg	gtt	tca	aat	tgc	ttg	ttc	816
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	
			260					265					270			
cgt	gtt	ggg	ggg	gcc	gct	att	ttg	ctc	tcc	aac	aag	cct	gga	gat	cgt	864
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	
			275				280					285				
aga	cgg	tcc	aag	tac	gag	cta	gtt	cac	acg	gtt	cga	acg	cat	acc	gga	912
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	
	290					295					300					
gct	gac	ggc	aag	tct	ttt	cgt	tgc	gtg	caa	caa	gga	gac	gat	gag	aac	960
Ala	Asp	Gly	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn	
305					310				315					320		
ggc	aaa	atc	gga	gtg	agt	ttg	tcc	aag	gac	ata	acc	gat	gtt	gct	ggg	1008
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly	
				325					330					335		
cga	acg	gtt	aag	aaa	aac	ata	gca	acg	ttg	ggg	ccg	ttg	att	ctt	ccg	1056
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro	
			340					345					350			
tta	agc	gag	aaa	ctt	ctt	ttt	ttc	gtt	acc	ttc	atg	ggc	aag	aaa	ctt	1104
Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu	
			355				360					365				
ttc	aaa	gat	aaa	atc	aaa	cat	tac	tac	gtc	ccg	gat	ttc	aaa	ctt	gct	1152
Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala	
	370					375					380					
att	gac	cat	ttt	tgt	ata	cat	gcc	gga	ggc	aga	gcc	gtg	att	gat	gtg	1200
Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val	
385					390					395				400		
cta	gag	aag	aac	cta	gcc	cta	gca	ccg	atc	gat	gta	gag	gca	tca	aga	1248
Leu	Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg	
			405						410					415		
tca	acg	tta	cat	aga	ttt	gga	aac	act	tca	tct	agc	tca	ata	tgg	tat	1296
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr	
			420					425					430			
gag	ttg	gca	tac	ata	gaa	gca	aaa	gga	agg	atg	aag	aaa	ggg	aat	aaa	1344
Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys	
			435				440					445				
gtt	tgg	cag	att	gct	tta	ggg	tca	ggc	ttt	aag	tgt	aac	agt	gca	gtt	1392
Val	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val	
	450					455					460					
tgg	gtg	gct	cta	aac	aat	gtc	aaa	gct	tcg	aca	aat	agt	cct	tgg	gaa	1440

Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu  
 465 470 475 480

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag 1488  
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys  
 485 490 495

tca gag act cgt gtc cca aac ggt cgg tcc taa 1521  
 Ser Glu Thr Arg Val Pro Asn Gly Arg Ser  
 500 505

<210> 12  
 <211> 506  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> 5' 114 amino acids from A. thaliana FAE1 (SEQ ID  
 NO:2) and 3' 392 amino acids from B. napus  
 elongase KCS (SEQ ID NO:4) having mutations at  
 residues 91 and 92; designated At114 L91C K92R

<400> 12  
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 1 5 10 15  
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys  
 20 25 30  
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu  
 35 40 45  
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe  
 50 55 60  
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val  
 65 70 75 80  
 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Cys Arg Val Ser Val Ser  
 85 90 95  
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser  
 100 105 110  
 Arg Asn Gly Thr Cys Asp Asn Ser Trp Leu Asp Phe Leu Arg Lys  
 115 120 125  
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly  
 130 135 140  
 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu  
 145 150 155 160  
 Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr  
 165 170 175  
 Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met  
 180 185 190  
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys  
 195 200 205  
 Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser  
 210 215 220  
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His  
 225 230 235 240  
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn  
 245 250 255

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Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
      260                      265                      270
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
      275                      280                      285
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
      290                      295                      300
Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
305                      310                      315                      320
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
      325                      330                      335
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
      340                      345                      350
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
      355                      360                      365
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
      370                      375                      380
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
385                      390                      395                      400
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
      405                      410                      415
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
      420                      425                      430
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
      435                      440                      445
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
      450                      455                      460
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
465                      470                      475                      480
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
      485                      490                      495
Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
      500                      505

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<210> 13

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and  
3' 1179 bp from B. napus elongase KCS (SEQ ID  
NO:3), having a mutation at position 275;  
designated At114 K92R

<221> CDS

<222> (1)...(1518)

<400> 13

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atg acg tcc gtt aac gtt aag ctc ctt tac cgt tat gtc tta acc aac      48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
  1                      5                      10                      15

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa      96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
      20                      25                      30

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gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	
ggc ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	
gac tac tcg tgt tac ctt ccg cca ccg cat ctc aga gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Arg Val Ser Val Ser	
85 90 95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	
cgg aac ggc acg tgt gat gat tcg tcg tgg ctt gac ttc ttg agg aag	384
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly	
130 135 140	
ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag	480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu	
145 150 155 160	
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc	528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	
165 170 175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg	576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt	672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat	720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	
245 250 255	

att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe 260 265 270	816
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg 275 280 285	864
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly 290 295 300	912
gct gac ggc aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn 305 310 315 320	960
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly 325 330 335	1008
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro 340 345 350	1056
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu 355 360 365	1104
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala 370 375 380	1152
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val 385 390 395 400	1200
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg 405 410 415	1248
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr 420 425 430	1296
gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys 435 440 445	1344
gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val 450 455 460	1392
tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Thr Asn Ser Pro Trp Glu 465 470 475 480	1440

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag      1488  
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys  
                485                         490                         495

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tca gag act cgt gtc cca aac ggt cgg tcc taa      1521
Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
          500                      505
```

<210> 14

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 114 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 392 amino acids from B. napus elongase KCS (SEQ ID NO:4), having a mutation at position 92; designated At114 K92R

<400> 14

Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn
1				5					10					15	
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys
			20					25				30			
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu
		35					40					45			
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe
	50					55				60					
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val
65					70					75					80
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Arg	Val	Ser	Val	Ser
				85					90					95	
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser
			100					105					110		
Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys
		115					120					125			
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly
	130					135					140				
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu
145					150					155					160
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr
				165					170					175	
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met
			180					185					190		
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys
		195					200					205			
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser
	210					215					220				
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His
225					230					235				240	
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn
				245					250					255	
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe
			260					265					270		
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg

275	280	285
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly		
290	295	300
Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn		
305	310	315
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly		
325	330	335
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro		
340	345	350
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu		
355	360	365
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala		
370	375	380
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val		
385	390	395
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg		
405	410	415
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr		
420	425	430
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys		
435	440	445
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val		
450	455	460
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu		
465	470	475
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys		
485	490	495
Ser Glu Thr Arg Val Pro Asn Gly Arg Ser		
500	505	

&lt;210&gt; 15

&lt;211&gt; 1521

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> 5' 342 bp from *A. thaliana* FAE1 (SEQ ID NO:1) and  
 3' 1179 bp from *B. napus* elongase KCS (SEQ ID  
 NO:3), having a mutation at position 920;  
 designated At114 G307D; hypothetical

&lt;221&gt; CDS

&lt;222&gt; (1)...(1518)

&lt;400&gt; 15

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tat gtc tta acc aac	48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn	
1 5 10 15	
ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa	96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	
ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	
gac tac tcg tgt tac ctt ccg cca ccg cat ctc aaa gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser	
85 90 95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	
cgg aac ggc acg tgt gat gat tcg tcg tgg ctt gac ttc ttg agg aag	384
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly	
130 135 140	
ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag	480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu	
145 150 155 160	
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc	528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	
165 170 175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg	576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt	672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat	720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	
245 250 255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc	816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	

cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt	864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg	
275 280 285	
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga	912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly	
290 295 300	
gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac	960
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn	
305 310 315 320	
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt	1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly	
325 330 335	
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg	1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	
340 345 350	
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt	1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu	
355 360 365	
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct	1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	
370 375 380	
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg	1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val	
385 390 395 400	
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga	1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg	
405 410 415	
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat	1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr	
420 425 430	
gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa	1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys	
435 440 445	
gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt	1392
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val	
450 455 460	
tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa	1440
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu	
465 470 475 480	
cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag	1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys	
485 490 495	

tca gag act cgt gtc caa aac ggt cgg tcc taa  
 Ser Glu Thr Arg Val Gln Asn Gly Arg Ser  
 500 505

1521

<210> 16  
 <211> 506  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> 5' 114 amino acids from A. thaliana FAE1 (SEQ ID  
 NO:2) and 3' 392 amino acids from B. napus  
 elongase KCS (SEQ ID NO:4) having mutation at  
 residue 307; designated At114 G307D; hypothetical

<400> 16  
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 1 5 10 15  
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys  
 20 25 30  
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu  
 35 40 45  
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe  
 50 55 60  
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val  
 65 70 75 80  
 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser  
 85 90 95  
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser  
 100 105 110  
 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys  
 115 120 125  
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly  
 130 135 140  
 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Arg Glu Glu  
 145 150 155 160  
 Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr  
 165 170 175  
 Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met  
 180 185 190  
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys  
 195 200 205  
 Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser  
 210 215 220  
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His  
 225 230 235 240  
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn  
 245 250 255  
 Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe  
 260 265 270  
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg  
 275 280 285  
 Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly  
 290 295 300

Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn  
 305 310 315 320  
 Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly  
 325 330 335  
 Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro  
 340 345 350  
 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu  
 355 360 365  
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala  
 370 375 380  
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val  
 385 390 395 400  
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg  
 405 410 415  
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr  
 420 425 430  
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys  
 435 440 445  
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val  
 450 455 460  
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu  
 465 470 475 480  
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys  
 485 490 495  
 Ser Glu Thr Arg Val Gln Asn Gly Arg Ser  
 500 505

<210> 17

<211> 1518

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 222 bp from A. thaliana FAE1 (SEQ ID NO:1) and  
 3' 1296 bp from B. napus elongase KCS (SEQ ID  
 NO:3) having a mutation at position 917;  
 designated At74 G306D; hypothetical

<221> CDS

<222> (1)...(1515)

<400> 17

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac	48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn	
1 5 10 15	
ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa	96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	



50	55	60	
ggt ttg gtt ctc tac atc gta acc cga ccc aaa ccg gtt tac ctc gtt			240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Lys Pro Val Tyr Leu Val			
65	70	75	80
gag tac tca tgc tac ctt cca cca acg cat tgt aga tca agt atc tcc			288
Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile Ser			
	85	90	95
aag gtc atg gat atc ttt tat caa gta aga aaa gct gat cct tct cgg			336
Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser Arg			
	100	105	110
aac ggc acg tgc gat gac tcg tcg tgg ctt gac ttc ttg agg aag att			384
Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys Ile			
	115	120	125
caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg ctg			432
Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly Leu			
	130	135	140
ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag acg			480
Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu Thr			
145	150	155	160
gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc aac			528
Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr Asn			
	165	170	175
gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg ttt			576
Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met Phe			
	180	185	190
aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag ctc			624
Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys Leu			
	195	200	205
cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt gcc			672
Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser Ala			
	210	215	220
ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat aaa			720
Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His Lys			
225	230	235	240
aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac att			768
Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn Ile			
	245	250	255
tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc cgt			816
Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe Arg			
	260	265	270
gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt aga			864
Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg Arg			

275	280	285	
cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga gct Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly Ala 290 295 300			912
gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac ggc Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn Gly 305 310 315 320			960
aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt cga Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly Arg 325 330 335			1008
acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg tta Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro Leu 340 345 350			1056
agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt ttc Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu Phe 355 360 365			1104
aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct att Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala Ile 370 375 380			1152
gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg cta Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val Leu 385 390 395 400			1200
gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga tca Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg Ser 405 410 415			1248
acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat gag Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr Glu 420 425 430			1296
ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa gtt Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys Val 435 440 445			1344
tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt tgg Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp 450 455 460			1392
gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa cac Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu His 465 470 475 480			1440
tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag tca Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys Ser 485 490 495			1488
gag act cgt gtc caa aac ggt cgg tcc taa Glu Thr Arg Val Gln Asn Gly Arg Ser			1518

500

505

<210> 18  
 <211> 505  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> 5' 74 amino acids from *A. thaliana* FAE1 (SEQ ID NO:2) and 3' 431 amino acids from *B. napus* elongase KCS (SEQ ID NO:4) having a mutation at residue 306; designated At74 G306D; hypothetical

<400> 18

Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn
1				5					10					15	
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys
		20						25				30			
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu
		35				40					45				
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe
	50					55				60					
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Lys	Pro	Val	Tyr	Leu	Val
65				70					75					80	
Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	His	Cys	Arg	Ser	Ser	Ile	Ser
			85					90						95	
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	Pro	Ser	Arg
			100					105				110			
Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys	Ile
		115				120					125				
Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly	Leu
	130					135					140				
Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu	Thr
145					150				155					160	
Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr	Asn
			165					170					175		
Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	Phe
			180					185					190		
Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	Leu
		195					200					205			
Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	Ala
	210					215					220				
Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	Lys
225				230					235					240	
Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	Ile
			245						250				255		
Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	Arg
			260				265					270			
Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	Arg
	275					280						285			
Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	Ala
	290					295					300				
Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn	Gly
305				310					315					320	
Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly	Arg

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          325          330          335
Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro Leu
          340          345          350
Ser Glu Lys Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu Phe
          355          360          365
Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala Ile
          370          375          380
Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val Leu
385          390          395          400
Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg Ser
          405          410          415
Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr Glu
          420          425          430
Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys Val
          435          440          445
Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp
          450          455          460
Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu His
465          470          475          480
Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys Ser
          485          490          495
Glu Thr Arg Val Gln Asn Gly Arg Ser
          500          505

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<210> 19

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and  
3' 1179 bp from B. napus elongase KCS (SEQ ID  
NO:3) having mutations at positions 271, 272, 275  
and 920; designated At114 L91C K92R G307D;  
hypothetical

<221> CDS

<222> (1)...(1518)

<400> 19

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atg acg tcc gtt aac gtt aag ctc ctt tac cgt tat gtc tta acc aac      48
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 1              5              10              15

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa      96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
          20              25              30

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc      144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
          35              40              45

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc      192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
          50              55              60

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ggt ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	
gac tac tcg tgt tac ctt ccg cca ccg cat tgc aga gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Cys Arg Val Ser Val Ser	
85 90 95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	
cgg aac ggc acg tgt gat aat tcg tcg tgg ctt gac ttc ttg agg aag	384
Arg Asn Gly Thr Cys Asp Asn Ser Ser Trp Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly	
130 135 140	
ctg ctt cag gtc cct ccc ccg aag act ttt gcg gcg gcg cgt gaa gag	480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu	
145 150 155 160	
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc	528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	
165 170 175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg	576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt	672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat	720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	
245 250 255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc	816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt	864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg	
275 280 285	

aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly 290 295 300	912
gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn 305 310 315 320	960
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly 325 330 335	1008
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro 340 345 350	1056
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu 355 360 365	1104
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala 370 375 380	1152
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val 385 390 395 400	1200
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg 405 410 415	1248
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr 420 425 430	1296
gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys 435 440 445	1344
gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val 450 455 460	1392
tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu 465 470 475 480	1440
cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys 485 490 495	1488
tca gag act cgt gtc caa aac ggt cgg tcc taa Ser Glu Thr Arg Val Gln Asn Gly Arg Ser 500 505	1521

<210> 20  
 <211> 506  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> 5' 114 amino acids from *A. thaliana* FAE1 (SEQ ID NO:2) and 3' 392 amino acids from *B. napus* elongase KCS (SEQ ID NO:4) having mutations at positions 91, 92 and 307; designated At114 L91C K92R G307D; hypothetical

<400> 20

Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn	1	5	10	15
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys	20	25	30	
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu	35	40	45	
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe	50	55	60	
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val	65	70	75	80
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Cys	Arg	Val	Ser	Val	Ser	85	90	95	
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser	100	105	110	
Arg	Asn	Gly	Thr	Cys	Asp	Asn	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys	115	120	125	
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly	130	135	140	
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu	145	150	155	160
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr	165	170	175	
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	180	185	190	
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	195	200	205	
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	210	215	220	
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	225	230	235	240
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	245	250	255	
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	260	265	270	
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	275	280	285	
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	290	295	300	
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn	305	310	315	320
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly	325	330	335	

Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro  
 340 345 350  
 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu  
 355 360 365  
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala  
 370 375 380  
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val  
 385 390 395 400  
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg  
 405 410 415  
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr  
 420 425 430  
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys  
 435 440 445  
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val  
 450 455 460  
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu  
 465 470 475 480  
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys  
 485 490 495  
 Ser Glu Thr Arg Val Gln Asn Gly Arg Ser  
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<210> 21

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and  
 3' 1179 bp from B. napus elongase KCS (SEQ ID  
 NO:3) having mutations at positions 275 and 920;  
 designated At114 K92R G307D; hypothetical

<221> CDS

<222> (1)...(1518)

<400> 21

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ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa 96  
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys  
 20 25 30

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc 144  
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu  
 35 40 45

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc 192  
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe  
 50 55 60

ggt ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt 240  
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val



65	70	75	80	
gac tac tcg tgt tac ctt ccg cca ccg cat ctc aga gtt agt gtc tct				288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Arg Val Ser Val Ser				
	85	90	95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca				336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser				
	100	105	110	
cgg aac ggc acg tgt gat gat tcg tcg tgg ctt gac ttc ttg agg aag				384
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys				
	115	120	125	
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg				432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly				
	130	135	140	
ctg ctt cag gtc cct ccc ccg aag act ttt gcg gcg gcg cgt gaa gag				480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu				
	145	150	155	160
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc				528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr				
	165	170	175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg				576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met				
	180	185	190	
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag				624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys				
	195	200	205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt				672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser				
	210	215	220	
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat				720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His				
	225	230	235	240
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac				768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn				
	245	250	255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc				816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe				
	260	265	270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt				864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg				
	275	280	285	
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga				912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly				

290	295	300	
gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac			960
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn			
305	310	315	320
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt			1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly			
	325	330	335
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg			1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro			
	340	345	350
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt			1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu			
	355	360	365
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct			1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala			
	370	375	380
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg			1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val			
385	390	395	400
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga			1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg			
	405	410	415
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat			1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr			
	420	425	430
gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa			1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys			
	435	440	445
gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt			1392
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val			
	450	455	460
tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa			1440
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu			
465	470	475	480
cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag			1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys			
	485	490	495
tca gag act cgt gtc caa aac ggt cgg tcc taa			1521
Ser Glu Thr Arg Val Gln Asn Gly Arg Ser			
	500	505	

<211> 506  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> 5' 114 amino acids from *A. thaliana* FAE1 (SEQ ID NO:2) and 3' 392 amino acids from *B. napus* elongase KCS (SEQ ID NO:4) having mutations at positions 92 and 307; designated At114 K92R G307D; hypothetical

<400> 22

Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn
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		20						25					30		
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu
		35					40					45			
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe
	50					55					60				
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val
65					70					75					80
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Arg	Val	Ser	Val	Ser
				85					90					95	
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser
			100					105					110		
Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys
	115						120					125			
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly
	130					135					140				
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu
145					150					155					160
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr
				165					170					175	
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met
		180					185						190		
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys
	195						200					205			
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser
	210					215					220				
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His
225					230					235					240
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn
				245					250					255	
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe
		260						265					270		
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg
	275						280					285			
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly
	290					295					300				
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn
305					310					315					320
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly
				325					330					335	
Arg	Thr	Val	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro	
			340				345						350		

Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu  
 355 360 365  
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala  
 370 375 380  
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val  
 385 390 395 400  
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg  
 405 410 415  
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr  
 420 425 430  
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys  
 435 440 445  
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val  
 450 455 460  
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu  
 465 470 475 480  
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys  
 485 490 495  
 Ser Glu Thr Arg Val Gln Asn Gly Arg Ser  
 500 505

<210> 23

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 762 bp from A. thaliana FAE1 (SEQ ID NO:1) and  
 3' 759 bp from B. napus elongase KCS (SEQ ID  
 NO:3); designated At254

<221> CDS

<222> (1)...(1518)

<400> 23

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac	48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn	
1 5 10 15	
ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa	96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	
ggt ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	
gac tac tcg tgt tac ctt cca cca ccg cat ctc aaa gtt agt gtc tct	288

Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Lys	Val	Ser	Val	Ser		
				85					90					95			
aaa	gtc	atg	gat	att	ttc	tac	caa	ata	aga	aaa	gct	gat	act	tct	tca		336
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser		
			100					105					110				
cgg	aac	gtg	gca	tgt	gat	gat	cgg	tcc	tcg	ctc	gat	ttc	ctg	agg	aag		384
Arg	Asn	Val	Ala	Cys	Asp	Asp	Pro	Ser	Ser	Leu	Asp	Phe	Leu	Arg	Lys		
		115					120					125					
att	caa	gag	cgt	tca	ggg	cta	ggg	gat	gag	acg	tac	agt	cct	gag	gga		432
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	Tyr	Ser	Pro	Glu	Gly		
	130					135					140						
ctc	att	cac	gta	cca	ccg	cgg	aag	act	ttt	gca	gcg	tca	cgt	gaa	gag		480
Leu	Ile	His	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ser	Arg	Glu	Glu		
145				150					155					160			
aca	gag	aag	gtt	atc	atc	ggg	gcg	ctc	gaa	aat	cta	ttc	gag	aac	acc		528
Thr	Glu	Lys	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Glu	Asn	Thr		
			165					170					175				
aaa	gtt	aac	cct	aga	gag	att	ggg	ata	ctt	gtg	gtg	aac	tca	agc	atg		576
Lys	Val	Asn	Pro	Arg	Glu	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met		
			180				185						190				
ttt	aat	cca	act	cct	tcg	cta	tcc	gct	atg	gtc	gtt	aat	act	ttc	aag		624
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys		
	195						200					205					
ctc	cga	agc	aac	atc	aaa	agc	ttt	aat	cta	gga	gga	atg	ggg	tgt	agt		672
Leu	Arg	Ser	Asn	Ile	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser		
	210					215					220						
gct	ggg	gtt	att	gcc	att	gat	ttg	gct	aaa	gac	ttg	ttg	cat	gtt	cat		720
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His		
225				230					235					240			
aaa	aac	act	tat	gct	ctc	gtg	gtg	agc	aca	gag	aac	atc	act	tat	aac		768
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn		
			245					250					255				
att	tac	gct	ggg	gat	aat	agg	tcc	atg	atg	gtt	tca	aat	tgc	ttg	ttc		816
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe		
		260					265					270					
cgt	gtt	ggg	ggg	gcc	gct	att	ttg	ctc	tcc	aac	aag	cct	gga	gat	cgt		864
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg		
		275				280						285					
aga	cgg	tcc	aag	tac	gag	cta	gtt	cac	acg	gtt	cga	acg	cat	acc	gga		912
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly		
	290					295					300						
gct	gac	ggc	aag	tct	ttt	cgt	tgc	gtg	caa	caa	gga	gac	gat	gag	aac		960

Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn	
305 310 315 320	
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt	1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly	
325 330 335	
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg	1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	
340 345 350	
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt	1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu	
355 360 365	
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct	1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	
370 375 380	
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg	1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val	
385 390 395 400	
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga	1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg	
405 410 415	
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat	1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr	
420 425 430	
gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa	1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys	
435 440 445	
gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt	1392
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val	
450 455 460	
tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa	1440
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu	
465 470 475 480	
cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag	1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys	
485 490 495	
tca gag act cgt gtc cca aac ggt cgg tcc taa	1521
Ser Glu Thr Arg Val Pro Asn Gly Arg Ser	
500 505	

&lt;210&gt; 24

&lt;211&gt; 506

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

**<220>**

<223> 5' 254 amino acids from *A. thaliana* FAE1 (SEQ ID NO:2) and 3' 252 amino acids from *B. napus* elongase KCS (SEQ ID NO:4); designated At254

<400> 24

Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn
1				5					10					15	
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys
			20					25					30		
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu
		35					40					45			
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe
	50					55				60					
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val
65				70					75						80
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Lys	Val	Ser	Val	Ser
			85					90					95		
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser
			100					105					110		
Arg	Asn	Val	Ala	Cys	Asp	Asp	Pro	Ser	Ser	Leu	Asp	Phe	Leu	Arg	Lys
		115					120					125			
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	Tyr	Ser	Pro	Glu	Gly
	130					135					140				
Leu	Ile	His	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ser	Arg	Glu	Glu
145				150					155						160
Thr	Glu	Lys	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Glu	Asn	Thr
			165						170					175	
Lys	Val	Asn	Pro	Arg	Glu	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met
			180					185					190		
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys
		195					200					205			
Leu	Arg	Ser	Asn	Ile	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser
	210					215					220				
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His
225				230					235						240
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn
			245						250					255	
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe
			260					265					270		
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg
		275					280					285			
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly
		290				295					300				
Ala	Asp	Gly	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn
305				310					315						320
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly
			325						330					335	
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro
			340					345					350		
Leu	Ser	Glu	Lys	Leu											

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385          390          395          400
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
          405          410          415
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
          420          425          430
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
          435          440          445
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
          450          455          460
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
465          470          475          480
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
          485          490          495
Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
          500          505

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<210> 25

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 519 bp from A. thaliana FAE1 (SEQ ID NO:1) and  
3' 1002 bp from B. napus elongase KCS (SEQ ID  
NO:3); designated At173

<221> CDS

<222> (1)...(1518)

<400> 25

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atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac      48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
  1              5              10              15

```

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ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa      96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
          20              25              30

```

```

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc     144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
          35              40              45

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caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc     192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
          50              55              60

```

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ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt     240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
          65              70              75              80

```

```

gac tac tcg tgt tac ctt cca cca ccg cat ctc aaa gtt agt gtc tct     288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser
          85              90              95

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aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca     336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser

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100	105	110	
cgg aac gtg gca tgt gat gat	cgg tcc tcg ctc gat ttc	ctg agg aag	384
Arg Asn Val Ala Cys Asp Asp	Pro Ser Ser Leu Asp Phe	Leu Arg Lys	
115	120	125	
att caa gag cgt tca ggt cta ggt	gat gag acg tac agt cct	gag gga	432
Ile Gln Glu Arg Ser Gly Leu	Gly Asp Glu Thr Tyr Ser	Pro Glu Gly	
130	135	140	
ctc att cac gta cca ccg cgg aag act	ttt gca gcg tca cgt gaa	gag	480
Leu Ile His Val Pro Pro Arg Lys	Thr Phe Ala Ala Ser Arg	Glu Glu	
145	150	155 160	
aca gag aag gtt atc atc ggt gcg ctc	gaa aat cta ttc aag aac acc		528
Thr Glu Lys Val Ile Ile Gly Ala	Leu Glu Asn Leu Phe Lys Asn	Thr	
165	170	175	
aac gtt aac cct aaa gat ata ggt	ata ctt gtg gtg aac tca agc atg		576
Asn Val Asn Pro Lys Asp Ile Gly	Ile Leu Val Val Asn Ser Ser	Met	
180	185	190	
ttt aat cca act cca tcg ctc tcc gcg	atg gtc gtt aac act ttc aag		624
Phe Asn Pro Thr Pro Ser Leu Ser	Ala Met Val Val Asn Thr Phe	Lys	
195	200	205	
ctc cga agc aac gta aga agc ttt aac	ctt ggt ggc atg ggt tgt agt		672
Leu Arg Ser Asn Val Arg Ser Phe	Asn Leu Gly Gly Met Gly Cys	Ser	
210	215	220	
gcc ggc gtt ata gcc att gat cta gca	aag gac ttg ttg cat gtc cat		720
Ala Gly Val Ile Ala Ile Asp Leu	Ala Lys Asp Leu Leu His Val	His	
225	230	235 240	
aaa aat acg tat gct ctt gtg gtg agc	aca gag aac atc act tat aac		768
Lys Asn Thr Tyr Ala Leu Val Val	Ser Thr Glu Asn Ile Thr Tyr	Asn	
245	250	255	
att tac gct ggt gat aat agg tcc atg	atg gtt tca aat tgc ttg ttc		816
Ile Tyr Ala Gly Asp Asn Arg Ser	Met Met Val Ser Asn Cys Leu	Phe	
260	265	270	
cgt gtt ggt ggg gcc gct att ttg ctc	tcc aac aag cct gga gat cgt		864
Arg Val Gly Gly Ala Ala Ile Leu	Leu Ser Asn Lys Pro Gly Asp	Arg	
275	280	285	
aga cgg tcc aag tac gag cta gtt cac	acg gtt cga acg cat acc gga		912
Arg Arg Ser Lys Tyr Glu Leu Val	His Thr Val Arg Thr His Thr	Gly	
290	295	300	
gct gac ggc aag tct ttt cgt tgc gtg	caa caa gga gac gat gag aac		960
Ala Asp Gly Lys Ser Phe Arg Cys	Val Gln Gln Gly Asp Asp Glu	Asn	
305	310	315 320	
ggc aaa atc gga gtg agt ttg tcc aag	gac ata acc gat gtt gct ggt		1008
Gly Lys Ile Gly Val Ser Leu Ser	Lys Asp Ile Thr Asp Val Ala	Gly	

325								330								335								
cga	acg	gtt	aag	aaa	aac	ata	gca	acg	ttg	ggg	ccg	ttg	att	ctt	ccg		1056							
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro									
340								345				350												
tta	agc	gag	aaa	ctt	ctt	ttt	ttc	gtt	acc	ttc	atg	ggc	aag	aaa	ctt		1104							
Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu									
355								360				365												
ttc	aaa	gat	aaa	atc	aaa	cat	tac	tac	gtc	ccg	gat	ttc	aaa	ctt	gct		1152							
Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala									
370								375				380												
att	gac	cat	ttt	tgt	ata	cat	gcc	gga	ggc	aga	gcc	gtg	att	gat	gtg		1200							
Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val									
385								390				395				400								
cta	gag	aag	aac	cta	gcc	cta	gca	ccg	atc	gat	gta	gag	gca	tca	aga		1248							
Leu	Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg									
				405								410				415								
tca	acg	tta	cat	aga	ttt	gga	aac	act	tca	tct	agc	tca	ata	tggt	tat		1296							
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr									
				420								425				430								
gag	ttg	gca	tac	ata	gaa	gca	aaa	gga	agg	atg	aag	aaa	ggg	aat	aaa		1344							
Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys									
435								440				445												
gtt	tggt	cag	att	gct	tta	ggg	tca	ggc	ttt	aag	tgt	aac	agt	gca	gtt		1392							
Val	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val									
450								455				460												
tggt	gtg	gct	cta	aac	aat	gtc	aaa	gct	tcg	aca	aat	agt	cct	tggt	gaa		1440							
Trp	Val	Ala	Leu	Asn	Asn	Val	Lys	Ala	Ser	Thr	Asn	Ser	Pro	Trp	Glu									
465								470				475				480								
cac	tgc	atc	gac	aga	tac	ccg	gtc	aaa	att	gat	tct	gat	tca	ggg	aag		1488							
His	Cys	Ile	Asp	Arg	Tyr	Pro	Val	Lys	Ile	Asp	Ser	Asp	Ser	Gly	Lys									
				485								490				495								
tca	gag	act	cgt	gtc	cma	aac	ggg	cgg	tcc	taa							1521							
Ser	Glu	Thr	Arg	Val	Xaa	Asn	Gly	Arg	Ser															
500								505																

&lt;210&gt; 26

&lt;211&gt; 506

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> 5' 173 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 333 amino acids from B. napus elongase KCS (SEQ ID NO:4); designated At173

&lt;221&gt; VARIANT

&lt;222&gt; (0)...(0)

&lt;223&gt; Xaa = Pro or Gln

&lt;400&gt; 26

Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn
1				5					10					15	
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys
		20					25					30			
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu
		35				40					45				
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe
	50				55					60					
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val
65				70					75					80	
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Lys	Val	Ser	Val	Ser
			85						90					95	
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser
		100					105					110			
Arg	Asn	Val	Ala	Cys	Asp	Asp	Pro	Ser	Ser	Leu	Asp	Phe	Leu	Arg	Lys
		115				120					125				
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	Tyr	Ser	Pro	Glu	Gly
	130				135				140						
Leu	Ile	His	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ser	Arg	Glu	Glu
145				150					155					160	
Thr	Glu	Lys	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr
			165			170						175			
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met
		180				185						190			
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys
		195				200						205			
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser
	210				215					220					
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His
225				230					235					240	
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn
			245					250					255		
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe
		260				265						270			
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	
	275					280					285				
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly
	290				295						300				
Ala	Asp	Gly	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn
305				310					315					320	
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly
			325					330					335		
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro
		340				345						350			
Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu
	355					360					365				
Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala
	370				375				380						
Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val
385				390					395					400	

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Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
      405      410      415
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr
      420      425      430
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
      435      440      445
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
      450      455      460
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
      465      470      475      480
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
      485      490      495
Ser Glu Thr Arg Val Xaa Asn Gly Arg Ser
      500      505

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<210> 27

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 528 bp from B. napus elongase KCS (SEQ ID NO:3)  
and 3' 993 bp from A. thaliana FAE1 (SEQ ID NO:1);  
designated Bn176

<221> CDS

<222> (1)...(1518)

<400> 27

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atg acg tcc att aac gta aag ctc ctt tac cat tac gtc ata acc aac      48
Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn
  1              5              10              15

ctt ttc aac ctt tgc ttc ttt ccg tta acg gcg atc gtc gcc gga aaa      96
Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
      20              25              30

gcc tat cgg ctt acc ata gac gat ctt cac cac tta tac tat tcc tat      144
Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
      35              40              45

ctc caa cac aac ctc ata acc atc gct cca ctc ttt gcc ttc acc gtt      192
Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
      50              55              60

ttc ggt tcg gtt ctc tac atc gca acc cgg ccc aaa ccg gtt tac ctc      240
Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
      65              70              75              80

gtt gag tac tca tgc tac ctt cca cca acg cat tgt aga tca agt atc      288
Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile
      85              90              95

tcc aag gtc atg gat atc ttt tat caa gta aga aaa gct gat cct tct      336
Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser
      100              105              110

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cgg aac ggc acg tgc gat gac tcg tcg tgg ctt gac ttc ttg agg aag Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys 115                                  120                                  125	384
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly 130                                  135                                  140	432
ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu 145                                  150                                  155                                  160	480
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr 165                                  170                                  175	528
aaa gtt aac cct aga gag att ggt ata ctt gtg gtg aac tca agc atg Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met 180                                  185                                  190	576
ttt aat cca act cct tcg cta tcc gct atg gtc gtt aat act ttc aag Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys 195                                  200                                  205	624
ctc cga agc aac atc aaa agc ttt aat cta gga gga atg ggt tgt agt Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser 210                                  215                                  220	672
gct ggt gtt att gcc att gat ttg gct aaa gac ttg ttg cat gtt cat Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His 225                                  230                                  235                                  240	720
aaa aac act tat gct ctt gtg gtg agc act gag aac atc aca caa ggc Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly 245                                  250                                  255	768
att tat gct gga gaa aat aga tca atg atg gtt agc aat tgc ttg ttt Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe 260                                  265                                  270	816
cgt gtt ggt ggg gcc gcg att ttg ctc tct aac aag tcg gga gac cgg Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg 275                                  280                                  285	864
aga cgg tcc aag tac aag cta gtt cac acg gtc cga acg cat act gga Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly 290                                  295                                  300	912
gct gat gac aag tct ttt cga tgt gtg caa caa gaa gat gat gag agc Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser 305                                  310                                  315                                  320	960
ggc aaa atc gga gtt tgt ctg tca aag gac ata acc aat gtt gcg ggg Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly 325                                  330                                  335	1008

aca aca ctt acg aaa aat ata gca aca ttg ggt ccg ttg att ctt cct	1056
Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	
340 345 350	
tta agc gaa aag ttt ctt ttt ttc gct acc ttc gtc gcc aag aaa ctt	1104
Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu	
355 360 365	
cta aag gat aaa atc aag cat tac tat gtt ccg gat ttc aag ctt gct	1152
Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	
370 375 380	
gtt gac cat ttc tgt att cat gcc gga ggc aga gcc gtg atc gat gag	1200
Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu	
385 390 395 400	
cta gag aag aac tta gga cta tcg ccg atc gat gtg gag gca tct aga	1248
Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg	
405 410 415	
tca acg tta cat aga ttt ggg aat act tca tct agc tca att tgg tat	1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr	
420 425 430	
gaa tta gca tac ata gag gca aag gga aga atg aag aaa ggg aat aaa	1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys	
435 440 445	
gct tgg cag att gct tta gga tca ggg ttt aag tgt aat agt gcg gtt	1392
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val	
450 455 460	
tgg gtg gct cta cgc aat gtc aag gca tcg gca aat agt cct tgg caa	1440
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln	
465 470 475 480	
cat tgc atc gat aga tat ccg gtt aaa att gat tct gat ttg tca aag	1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys	
485 490 495	
tca aag act cat gtc caa aac ggt cgg tcc taa	1521
Ser Lys Thr His Val Gln Asn Gly Arg Ser	
500 505	

&lt;210&gt; 28

&lt;211&gt; 506

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> 5' 176 amino acids from B. napus elongase KCS (SEQ ID NO:4) and 3' 330 amino acids from A. thaliana FAE1 (SEQ ID NO:2); designated Bn176

&lt;400&gt; 28

Met	Thr	Ser	Ile	Asn	Val	Lys	Leu	Leu	Tyr	His	Tyr	Val	Ile	Thr	Asn
1				5					10					15	
Leu	Phe	Asn	Leu	Cys	Phe	Phe	Pro	Leu	Thr	Ala	Ile	Val	Ala	Gly	Lys
			20					25					30		
Ala	Tyr	Arg	Leu	Thr	Ile	Asp	Asp	Leu	His	His	Leu	Tyr	Tyr	Ser	Tyr
		35					40					45			
Leu	Gln	His	Asn	Leu	Ile	Thr	Ile	Ala	Pro	Leu	Phe	Ala	Phe	Thr	Val
	50					55					60				
Phe	Gly	Ser	Val	Leu	Tyr	Ile	Ala	Thr	Arg	Pro	Lys	Pro	Val	Tyr	Leu
65					70				75						80
Val	Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	His	Cys	Arg	Ser	Ser	Ile
				85					90					95	
Ser	Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	Pro	Ser
			100					105					110		
Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys
		115					120					125			
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly
	130					135					140				
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu
145					150				155						160
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr
				165					170					175	
Lys	Val	Asn	Pro	Arg	Glu	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met
			180					185					190		
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys
	195						200					205			
Leu	Arg	Ser	Asn	Ile	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser
	210				215						220				
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His
225					230				235						240
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Gln	Gly
				245					250					255	
Ile	Tyr	Ala	Gly	Glu	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe
		260						265					270		
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Ser	Gly	Asp	Arg
	275						280						285		
Arg	Arg	Ser	Lys	Tyr	Lys	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly
	290				295						300				
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Glu	Asp	Asp	Glu	Ser
305					310				315						320
Gly	Lys	Ile	Gly	Val	Cys	Leu	Ser	Lys	Asp	Ile	Thr	Asn	Val	Ala	Gly
				325					330					335	
Thr	Thr	Leu	Thr	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro
			340					345					350		
Leu	Ser	Glu	Lys	Phe	Leu	Phe	Phe	Ala	Thr	Phe	Val	Ala	Lys	Lys	Leu
	355						360					365			
Leu	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala
	370				375						380				
Val	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Glu
385					390				395						400
Leu	Glu	Lys	Asn	Leu	Gly	Leu	Ser	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg
			405						410					415	
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr
			420					425					430		
Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys

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      435              440              445
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
      450              455              460
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln
465              470              475              480
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys
      485              490              495
Ser Lys Thr His Val Gln Asn Gly Arg Ser
      500              505

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<210> 29  
 <211> 1521  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> 5' 1197 bp from A. thaliana FAE1 (SEQ ID NO:1) and  
 3' 324 bp from B. napus elongase KCS (SEQ ID  
 NO:3); designated At399

<221> CDS  
 <222> (1) ... (1518)

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<400> 29
atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac      48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
  1              5              10              15

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa      96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
      20              25              30

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc      144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
      35              40              45

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc      192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
      50              55              60

ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt      240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
      65              70              75              80

gac tac tcg tgt tac ctt cca cca ccg cat ctc aaa gtt agt gtc tct      288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser
      85              90              95

aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca      336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
      100              105              110

cgg aac gtg gca tgt gat gat ccg tcc tcg ctc gat ttc ctg agg aag      384
Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys
      115              120              125

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att caa gag cgt tca ggt cta ggt gat gag acg tac agt cct gag gga Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly 130 135 140	432
ctc att cac gta cca ccg cgg aag act ttt gca gcg tca cgt gaa gag Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu 145 150 155 160	480
aca gag aag gtt atc atc ggt gcg ctc gaa aat cta ttc gag aac acc Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr 165 170 175	528
aaa gtt aac cct aga gag att ggt ata ctt gtg gtg aac tca agc atg Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met 180 185 190	576
ttt aat cca act cct tcg cta tcc gct atg gtc gtt aat act ttc aag Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys 195 200 205	624
ctc cga agc aac atc aaa agc ttt aat cta gga gga atg ggt tgt agt Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser 210 215 220	672
gct ggt gtt att gcc att gat ttg gct aaa gac ttg ttg cat gtt cat Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His 225 230 235 240	720
aaa aac act tat gct ctt gtg gtg agc act gag aac atc aca caa ggc Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly 245 250 255	768
att tat gct gga gaa aat aga tca atg atg gtt agc aat tgc ttg ttt Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe 260 265 270	816
cgt gtt ggt ggg gcc gcg att ttg ctc tct aac aag tcg gga gac cgg Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg 275 280 285	864
aga cgg tcc aag tac aag cta gtt cac acg gtc cga acg cat act gga Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly 290 295 300	912
gct gat gac aag tct ttt cga tgt gtg caa caa gaa gac gat gag agc Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser 305 310 315 320	960
ggc aaa atc gga gtt tgt ctg tca aag gac ata acc aat gtt gcg ggg Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly 325 330 335	1008
aca aca ctt acg aaa aat ata gca aca ttg ggt ccg ttg att ctt cct Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro 340 345 350	1056

tta agc gaa aag ttt ctt ttt ttc gct acc ttc gtc gcc aag aaa ctt	1104
Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu	
355 360 365	
cta aag gat aaa atc aag cat tac tat gtt ccg gat ttc aag ctt gct	1152
Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	
370 375 380	
gtt gac cat ttc tgt att cat gcc gga ggc aga gcc gtg atc gat gtg	1200
Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val	
385 390 395 400	
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga	1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg	
405 410 415	
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat	1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr	
420 425 430	
gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa	1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys	
435 440 445	
gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt	1392
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val	
450 455 460	
tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa	1440
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu	
465 470 475 480	
cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag	1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys	
485 490 495	
tca gag act cgt gtc cma aac ggt cgg tcc taa	1521
Ser Glu Thr Arg Val Xaa Asn Gly Arg Ser	
500 505	

&lt;210&gt; 30

&lt;211&gt; 506

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> 5' 399 amino acids from *A. thaliana* FAE1 (SEQ ID NO:2) and 3' 107 amino acids from *B. napus* elongase KCS (SEQ ID NO:4); designated At399

&lt;221&gt; VARIANT

&lt;222&gt; (0)...(0)

&lt;223&gt; Xaa = Pro or Gln

&lt;400&gt; 30

Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn	1	5	10	15
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys	20	25	30	
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu	35	40	45	
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe	50	55	60	
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val	65	70	75	80
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Lys	Val	Ser	Val	Ser	85	90	95	
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser	100	105	110	
Arg	Asn	Val	Ala	Cys	Asp	Asp	Pro	Ser	Ser	Leu	Asp	Phe	Leu	Arg	Lys	115	120	125	
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	Tyr	Ser	Pro	Glu	Gly	130	135	140	
Leu	Ile	His	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ser	Arg	Glu	Glu	145	150	155	160
Thr	Glu	Lys	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Glu	Asn	Thr	165	170	175	
Lys	Val	Asn	Pro	Arg	Glu	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	180	185	190	
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	195	200	205	
Leu	Arg	Ser	Asn	Ile	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	210	215	220	
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	225	230	235	240
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Gln	Gly	245	250	255	
Ile	Tyr	Ala	Gly	Glu	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	260	265	270	
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Ser	Gly	Asp	Arg	275	280	285	
Arg	Arg	Ser	Lys	Tyr	Lys	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	290	295	300	
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Glu	Asp	Asp	Glu	Ser	305	310	315	320
Gly	Lys	Ile	Gly	Val	Cys	Leu	Ser	Lys	Asp	Ile	Thr	Asn	Val	Ala	Gly	325	330	335	
Thr	Thr	Leu	Thr	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro	340	345	350	
Leu	Ser	Glu	Lys	Phe	Leu	Phe	Phe	Ala	Thr	Phe	Val	Ala	Lys	Lys	Leu	355	360	365	
Leu	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala	370	375	380	
Val	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val	385	390	395	400
Leu	Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg	405	410	415	
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr	420	425	430	
Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys	435	440	445	

Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val  
 450 455 460  
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu  
 465 470 475 480  
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys  
 485 490 495  
 Ser Glu Thr Arg Val Xaa Asn Gly Arg Ser  
 500 505

<210> 31  
 <211> 1521  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> 5' 1197 bp from B. napus elongase KCS (SEQ ID  
 NO:3) and 3' 324 bp from A. thaliana FAE1 (SEQ ID  
 NO:1); designated Bn399

<221> CDS  
 <222> (1)...(1518)

<400> 31  
 atg acg tcc att aac gtt aag ctc ctt tac cat tac gtc ata acc aac 48  
 Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn  
 1 5 10 15  
 ctt ttc aac ctt tgc ttc ttt ccg tta acg gcg atc gtc gcc gga aaa 96  
 Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys  
 20 25 30  
 gcc tat cgg ctt acc ata gac gat ctt cac cac tta tac tat tcc tat 144  
 Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr  
 35 40 45  
 ctc caa cac aac ctc ata acc atc gct cca ctc ttt gcc ttc acc gtt 192  
 Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val  
 50 55 60  
 ttc ggt tcg gtt ctc tac atc gca acc cgg ccc aaa ccg gtt tac ctc 240  
 Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu  
 65 70 75 80  
 gtt gag tac tca tgc tac ctt cca cca acg cat tgt aga tca agt atc 288  
 Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile  
 85 90 95  
 tcc aag gtc atg gat atc ttt tat caa gta aga aaa gct gat cct tct 336  
 Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser  
 100 105 110  
 cgg aac ggc acg tgc gat gac tcg tcg tgg ctt gac ttc ttg agg aag 384  
 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys  
 115 120 125  
 att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg 432

Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly	
130						135					140					
ctg	ctt	cag	gtc	cct	ccc	cgg	aag	act	ttt	gcg	gcg	gcg	cgt	gaa	gag	480
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu	
145					150					155					160	
acg	gag	caa	gtt	atc	att	ggg	gcg	cta	gaa	aat	cta	ttc	aag	aac	acc	528
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr	
				165					170					175		
aac	gtt	aac	cct	aaa	gat	ata	ggg	ata	ctt	gtg	gtg	aac	tca	agc	atg	576
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	
			180					185					190			
ttt	aat	cca	act	cca	tcg	ctc	tcc	gcg	atg	gtc	gtt	aac	act	ttc	aag	624
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	
		195					200					205				
ctc	cga	agc	aac	gta	aga	agc	ttt	aac	ctt	ggg	ggc	atg	ggg	tgt	agt	672
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	
	210					215					220					
gcc	ggc	gtt	ata	gcc	att	gat	cta	gca	aag	gac	ttg	ttg	cat	gtc	cat	720
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	
225					230					235					240	
aaa	aat	acg	tat	gct	ctt	gtg	gtg	agc	aca	gag	aac	atc	act	tat	aac	768
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	
				245					250					255		
att	tac	gct	ggg	gat	aat	agg	tcc	atg	atg	gtt	tca	aat	tgc	ttg	ttc	816
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	
			260					265					270			
cgt	gtt	ggg	ggg	gcc	gct	att	ttg	ctc	tcc	aac	aag	cct	gga	gat	cgt	864
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	
		275					280					285				
aga	cgg	tcc	aag	tac	gag	cta	gtt	cac	acg	gtt	cga	acg	cat	acc	gga	912
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	
		290				295					300					
gct	gac	ggc	aag	tct	ttt	cgt	tgc	gtg	caa	caa	gga	gac	gat	gag	aac	960
Ala	Asp	Gly	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn	
305					310					315					320	
ggc	aaa	atc	gga	gtg	agt	ttg	tcc	aag	gac	ata	acc	gat	gtt	gct	ggg	1008
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly	
				325					330					335		
cga	acg	gtt	aag	aaa	aac	ata	gca	acg	ttg	ggg	ccg	ttg	att	ctt	ccg	1056
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro	
			340					345					350			
tta	agc	gag	aaa	ctt	ctt	ttt	ttc	gtt	acc	ttc	atg	ggc	aag	aaa	ctt	1104

Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu  
 355 360 365  
 ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct 1152  
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala  
 370 375 380  
 att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg atc gat gag 1200  
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu  
 385 390 395 400  
 cta gag aag aac tta gga cta tcg ccg atc gat gtg gag gca tct aga 1248  
 Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg  
 405 410 415  
 tca acg tta cat aga ttt ggg aat act tca tct agc tca att tgg tat 1296  
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr  
 420 425 430  
 gaa tta gca tac ata gag gca aag gga aga atg aag aaa ggg aat aaa 1344  
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys  
 435 440 445  
 gct tgg cag att gct tta gga tca ggg ttt aag tgt aat agt gcg gtt 1392  
 Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val  
 450 455 460  
 tgg gtg gct cta cgc aat gtc aag gca tcg gca aat agt cct tgg caa 1440  
 Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln  
 465 470 475 480  
 cat tgc atc gat aga tat ccg gtt aaa att gat tct gat ttg tca aag 1488  
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys  
 485 490 495  
 tca aag act cat gtc caa aac ggt cgg tcc taa 1521  
 Ser Lys Thr His Val Gln Asn Gly Arg Ser  
 500 505

<210> 32

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 399 amino acids from B. napus elongase KCS (SEQ  
 ID NO:3) and 3' 107 amino acids from A. thaliana  
 FAE1 (SEQ ID NO:1); designated Bn399

<400> 32

Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn  
 1 5 10 15  
 Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys  
 20 25 30  
 Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr

35	40	45
Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val		
50	55	60
Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu		
65	70	75
Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile		80
85	90	95
Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser		
100	105	110
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys		
115	120	125
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly		
130	135	140
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu		
145	150	155
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr		160
165	170	175
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met		
180	185	190
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys		
195	200	205
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser		
210	215	220
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His		
225	230	235
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn		240
245	250	255
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe		
260	265	270
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg		
275	280	285
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly		
290	295	300
Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn		
305	310	315
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly		320
325	330	335
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro		
340	345	350
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu		
355	360	365
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala		
370	375	380
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu		
385	390	395
Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg		400
405	410	415
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr		
420	425	430
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys		
435	440	445
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val		
450	455	460
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln		
465	470	475
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys		480

485 490 495  
 Ser Lys Thr His Val Gln Asn Gly Arg Ser  
 500 505

```
<210> 33
<211> 1524
<212> DNA
<213> Artificial Sequence
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<220>
<223> 1524 bp from B. napus elongase KCS (SEQ ID NO:3)
      having a mutation at position 920; designated Bn
      G307D; hypothetical
```

<221> CDS  
<222> (1) ... (1518)

<400> 33																	
atg	acg	tcc	att	aac	gta	aag	ctc	ctt	tac	cat	tac	gtc	ata	acc	aac		48
Met	Thr	Ser	Ile	Asn	Val	Lys	Leu	Leu	Tyr	His	Tyr	Val	Ile	Thr	Asn		
1				5				10				15					
ctt	ttc	aac	ctt	tgc	ttc	ttt	ccg	tta	acg	gcg	atc	gtc	gcc	gga	aaa		96
Leu	Phe	Asn	Leu	Cys	Phe	Phe	Pro	Leu	Thr	Ala	Ile	Val	Ala	Gly	Lys		
20				25				30									
gcc	tat	cgg	ctt	acc	ata	gac	gat	ctt	cac	cac	tta	tac	tat	tcc	tat		144
Ala	Tyr	Arg	Leu	Thr	Ile	Asp	Asp	Leu	His	His	Leu	Tyr	Tyr	Ser	Tyr		
35				40				45									
ctc	caa	cac	aac	ctc	ata	acc	atc	gct	cca	ctc	ttt	gcc	ttc	acc	gtt		192
Leu	Gln	His	Asn	Leu	Ile	Thr	Ile	Ala	Pro	Leu	Phe	Ala	Phe	Thr	Val		
50				55				60									
ttc	ggg	tcg	gtt	ctc	tac	atc	gca	acc	cgg	ccc	aaa	ccg	gtt	tac	ctc		240
Phe	Gly	Ser	Val	Leu	Tyr	Ile	Ala	Thr	Arg	Pro	Lys	Pro	Val	Tyr	Leu		
65				70				75				80					
gtt	gag	tac	tca	tgc	tac	ctt	cca	cca	acg	cat	tgt	aga	tca	agt	atc		288
Val	Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	His	Cys	Arg	Ser	Ser	Ile		
85				90				95									
tcc	aag	gtc	atg	gat	atc	ttt	tat	caa	gta	aga	aaa	gct	gat	cct	tct		336
Ser	Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	Pro	Ser		
100				105				110									
cgg	aac	ggc	acg	tgc	gat	gac	tcg	tcg	tgg	ctt	gac	ttc	ttg	agg	aag		384
Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys		
115				120				125									
att	caa	gaa	cgt	tca	ggg	cta	ggc	gat	gaa	act	cac	ggg	ccc	gag	ggg		432
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly		
130				135				140									
ctg	ctt	cag	gtc	cct	ccc	cgg	aag	act	ttt	gcg	gcg	gcg	cgt	gaa	gag		480
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu		



145	150	155	160	
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc				528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	165	170	175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg				576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	180	185	190	
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag				624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	195	200	205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt				672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	210	215	220	
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat				720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	225	230	235	240
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac				768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	245	250	255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc				816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	260	265	270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt				864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg	275	280	285	
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga				912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly	290	295	300	
gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac				960
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn	305	310	315	320
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt				1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly	325	330	335	
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg				1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	340	345	350	
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt				1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu	355	360	365	
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct				1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala				

370	375	380	
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg			1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val			
385	390	395	400
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga			1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg			
	405	410	415
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat			1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr			
	420	425	430
gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa			1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys			
	435	440	445
gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt			1392
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val			
	450	455	460
tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa			1440
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu			
	465	470	475
cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag			1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys			
	485	490	495
tca gag act cgt gtc caa aac ggt cgg tcc taataa			1524
Ser Glu Thr Arg Val Gln Asn Gly Arg Ser			
	500	505	

&lt;210&gt; 34

&lt;211&gt; 506

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> 506 amino acids from B. napus elongase KCS (SEQ ID NO:4) having a mutation at residue 307; designated Bn G307D; hypothetical

&lt;400&gt; 34

Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn			
1	5	10	15
Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys			
	20	25	30
Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr			
	35	40	45
Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val			
	50	55	60
Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu			
65	70	75	80

Val	Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	His	Cys	Arg	Ser	Ser	Ile	
				85					90					95		
Ser	Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	Pro	Ser	
			100					105					110			
Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys	
		115					120					125				
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly	
	130					135					140					
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu	
145				150					155					160		
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr	
			165					170						175		
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	
			180				185						190			
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	
	195						200						205			
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	
	210					215						220				
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	
225				230					235					240		
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	
			245					250						255		
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	
		260						265					270			
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	
		275					280						285			
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	
	290				295						300					
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn	
305				310					315					320		
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly	
			325					330						335		
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro	
		340					345						350			
Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu	
	355					360						365				
Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala	
	370				375						380					
Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val	
385				390					395					400		
Leu	Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg	
			405					410					415			
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr	
		420						425					430			
Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys	
	435					440						445				
Val	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val	
	450				455						460					
Trp	Val	Ala	Leu	Asn	Asn	Val	Lys	Ala	Ser	Thr	Asn	Ser	Pro	Trp	Glu	
465				470					475					480		
His	Cys	Ile	Asp	Arg	Tyr	Pro	Val	Lys	Ile	Asp	Ser	Asp	Ser	Gly	Lys	
			485					490						495		
Ser	Glu	Thr	Arg	Val	Gln	Asn	Gly	Arg	Ser							
			500				505									

&lt;211&gt; 1709

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> 1709 bp from A. thaliana FAE1 (SEQ ID NO:1) having  
a mutation at position 275; designated At K92R;  
hypothetical

&lt;221&gt; CDS

&lt;222&gt; (1)...(1518)

&lt;400&gt; 35

atg	acg	tcc	ggt	aac	ggt	aag	ctc	ctt	tac	cgt	tac	gtc	tta	acc	aac	48
Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn	
1				5					10					15		

ttt	ttc	aac	ctc	tgt	ttg	ttc	ccg	tta	acg	gcg	ttc	ctc	gcc	gga	aaa	96
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys	
			20					25					30			

gcc	tct	cgg	ctt	acc	ata	aac	gat	ctc	cac	aac	ttc	ctt	tcc	tat	ctc	144
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu	
		35					40					45				

caa	cac	aac	ctt	ata	aca	gta	act	tta	ctc	ttt	gct	ttc	act	ggt	ttc	192
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe	
	50					55				60						

ggt	ttg	ggt	ctc	tac	atc	gta	acc	cga	ccc	aat	ccg	ggt	tat	ctc	ggt	240
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val	
65					70					75					80	

gac	tac	tcg	tgt	tac	ctt	cca	cca	ccg	cat	ctc	aga	ggt	agt	gtc	tct	288
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Arg	Val	Ser	Val	Ser	
			85						90					95		

aaa	gtc	atg	gat	att	ttc	tac	caa	ata	aga	aaa	gct	gat	act	tct	tca	336
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser	
			100					105					110			

cgg	aac	gtg	gca	tgt	gat	gat	ccg	tcc	tcg	ctc	gat	ttc	ctg	agg	aag	384
Arg	Asn	Val	Ala	Cys	Asp	Asp	Pro	Ser	Ser	Leu	Asp	Phe	Leu	Arg	Lys	
		115					120					125				

att	caa	gag	cgt	tca	ggt	cta	ggt	gat	gag	acg	tac	agt	cct	gag	gga	432
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	Tyr	Ser	Pro	Glu	Gly	
	130					135					140					

ctc	att	cac	gta	cca	ccg	cgg	aag	act	ttt	gca	gcg	tca	cgt	gaa	gag	480
Leu	Ile	His	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ser	Arg	Glu	Glu	
145					150					155				160		

aca	gag	aag	ggt	atc	atc	ggt	gcg	ctc	gaa	aat	cta	ttc	gag	aac	acc	528
Thr	Glu	Lys	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Glu	Asn	Thr	
				165				170						175		

aaa gtt aac cct aga gag att ggt ata ctt gtg gtg aac tca agc atg Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met	576
180 185 190	
ttt aat cca act cct tcg cta tcc gct atg gtc gtt aat act ttc aag Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	624
195 200 205	
ctc cga agc aac atc aaa agc ttt aat cta gga gga atg ggt tgt agt Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	672
210 215 220	
gct ggt gtt att gcc att gat ttg gct aaa gac ttg ttg cat gtt cat Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	720
225 230 235 240	
aaa aac act tat gct ctt gtg gtg agc act gag aac atc aca caa ggc Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly	768
245 250 255	
att tat gct gga gaa aat aga tca atg atg gtt agc aat tgc ttg ttt Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	816
260 265 270	
cgt gtt ggt ggg gcc gcg att ttg ctc tct aac aag tcg gga gac cgg Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg	864
275 280 285	
aga cgg tcc aag tac aag cta gtt cac acg gtc cga acg cat act gga Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly	912
290 295 300	
gct gat gac aag tct ttt cga tgt gtg caa caa gaa gac gat gag agc Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser	960
305 310 315 320	
ggc aaa atc gga gtt tgt ctg tca aag gac ata acc aat gtt gcg ggg Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly	1008
325 330 335	
aca aca ctt acg aaa aat ata gca aca ttg ggt ccg ttg att ctt cct Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	1056
340 345 350	
tta agc gaa aag ttt ctt ttt ttc gct acc ttc gtc gcc aag aaa ctt Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu	1104
355 360 365	
cta aag gat aaa atc aag cat tac tat gtt ccg gat ttc aag ctt gct Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	1152
370 375 380	
ggt gac cat ttc tgt att cat gcc gga ggc aga gcc gtg atc gat gag Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu	1200
385 390 395 400	

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cta gag aag aac tta gga cta tcg ccg atc gat gtg gag gca tct aga      1248
Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg
                405                      410                      415

tca acg tta cat aga ttt ggg aat act tca tct agc tca att tgg tat      1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
                420                      425                      430

gaa tta gca tac ata gag gca aag gga aga atg aag aaa ggg aat aaa      1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
                435                      440                      445

gct tgg cag att gct tta gga tca ggg ttt aag tgt aat agt gcg gtt      1392
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
                450                      455                      460

tgg gtg gct cta cgc aat gtc aag gca tcg gca aat agt cct tgg caa      1440
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln
                465                      470                      475                      480

cat tgc atc gat aga tat ccg gtt aaa att gat tct gat ttg tca aag      1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys
                485                      490                      495

tca aag act cat gtc caa aac ggt cgg tcc taatttgatg tatctgagtg      1538
Ser Lys Thr His Val Gln Asn Gly Arg Ser
                500                      505

ccaacggttta ctttgtcttt cctttctttt attgggttatg aattagatgt ttactaatgt      1598
tcctctctttt ttcgttataa ataaagaagt tcaattcttc ctatagtttc aaacgcgatt      1658
ttaagcgttt ctatttaggt ttacatgaat ttcttttaca aaccatcttt t      1709

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&lt;210&gt; 36

&lt;211&gt; 506

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> 506 amino acids from *A. thaliana* FAE1 (SEQ ID  
 NO:2) having a mutation at residue 92; designated  
 At K92R; hypothetical

&lt;400&gt; 36

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Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1                5                10                15
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
                20                25                30
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
                35                40                45
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50                55                60
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65                70                75                80
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Arg Val Ser Val Ser
                85                90                95

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Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser  
 100 105 110  
 Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys  
 115 120 125  
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly  
 130 135 140  
 Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu  
 145 150 155 160  
 Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr  
 165 170 175  
 Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met  
 180 185 190  
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys  
 195 200 205  
 Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser  
 210 215 220  
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His  
 225 230 235 240  
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly  
 245 250 255  
 Ile Tyr Ala Gly Glu Asn Arg Ser Met Val Ser Asn Cys Leu Phe  
 260 265 270  
 Arg Val Gly Gly Ala Ala Ile Leu Ser Asn Lys Ser Gly Asp Arg  
 275 280 285  
 Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly  
 290 295 300  
 Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser  
 305 310 315 320  
 Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly  
 325 330 335  
 Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro  
 340 345 350  
 Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu  
 355 360 365  
 Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala  
 370 375 380  
 Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu  
 385 390 395 400  
 Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg  
 405 410 415  
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr  
 420 425 430  
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys  
 435 440 445  
 Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val  
 450 455 460  
 Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln  
 465 470 475 480  
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys  
 485 490 495  
 Ser Lys Thr His Val Gln Asn Gly Arg Ser  
 500 505

&lt;210&gt; 37

&lt;211&gt; 1521

&lt;212&gt; DNA

## &lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> 5' 762 bp from *A. thaliana* FAE1 (SEQ ID NO:1) and  
 3' 759 bp from *B. napus* elongase KCS (SEQ ID NO:3)  
 and having a mutation at position 920; designated  
 At254 G307D; hypothetical

&lt;221&gt; CDS

&lt;222&gt; (1)...(1518)

&lt;400&gt; 37

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac	48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn	
1 5 10 15	
ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa	96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	
ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	
gac tac tcg tgt tac ctt cca cca ccg cat ctc aaa gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser	
85 90 95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	
cgg aac gtg gca tgt gat gat ccg tcc tcg ctc gat ttc ctg agg aag	384
Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gag cgt tca ggt cta ggt gat gag acg tac agt cct gag gga	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly	
130 135 140	
ctc att cac gta cca ccg cgg aag act ttt gca gcg tca cgt gaa gag	480
Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu	
145 150 155 160	
aca gag aag gtt atc atc ggt gcg ctc gaa aat cta ttc gag aac acc	528
Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr	
165 170 175	



aaa gtt aac cct aga gag att ggt ata ctt gtg gtg aac tca agc atg Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met	576
180 185 190	
ttt aat cca act cct tcg cta tcc gct atg gtc gtt aat act ttc aag Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	624
195 200 205	
ctc cga agc aac atc aaa agc ttt aat cta gga gga atg ggt tgt agt Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	672
210 215 220	
gct ggt gtt att gcc att gat ttg gct aaa gac ttg ttg cat gtt cat Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	720
225 230 235 240	
aaa aac act tat gct ctc gtg gtg agc aca gag aac atc act tat aac Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	768
245 250 255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	816
260 265 270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg	864
275 280 285	
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly	912
290 295 300	
gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn	960
305 310 315 320	
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly	1008
325 330 335	
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	1056
340 345 350	
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu	1104
355 360 365	
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	1152
370 375 380	
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val	1200
385 390 395 400	

cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga 1248  
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg  
                   405                  410                  415

tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat 1296  
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr  
                   420                  425                  430

gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa 1344  
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys  
                   435                  440                  445

gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt 1392  
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val  
                   450                  455                  460

tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa 1440  
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu  
                   465                  470                  475                  480

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag 1488  
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys  
                   485                  490                  495

tca gag act cgt gtc caa aac ggt cgg tcc taa 1521  
 Ser Glu Thr Arg Val Gln Asn Gly Arg Ser  
                   500                  505

<210> 38

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 254 amino acids from A. thaliana FAE1 (SEQ ID  
 NO:2) and 3' 252 amino acids from B. napus  
 elongase KCS (SEQ ID NO:4) having a mutation at  
 residue 307; designated At254 G307D; hypothetical

<400> 38

Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn  
 1                  5                  10                  15  
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys  
                   20                  25                  30  
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu  
                   35                  40                  45  
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe  
                   50                  55                  60  
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val  
 65                  70                  75                  80  
 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser  
                   85                  90                  95  
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser  
                   100                  105                  110  
 Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys

		115					120					125				
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	Tyr	Ser	Pro	Glu	Gly	
	130					135					140					
Leu	Ile	His	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ser	Arg	Glu	Glu	
145					150				155						160	
Thr	Glu	Lys	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Glu	Asn	Thr	
				165					170					175		
Lys	Val	Asn	Pro	Arg	Glu	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	
			180					185					190			
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	
		195					200					205				
Leu	Arg	Ser	Asn	Ile	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	
	210					215					220					
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	
225					230					235					240	
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	
				245					250					255		
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	
			260					265					270			
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	
		275					280					285				
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	
	290					295					300					
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn	
305					310					315					320	
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly	
				325					330					335		
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro	
			340					345					350			
Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu	
		355				360						365				
Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala	
	370					375					380					
Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val	
385					390					395					400	
Leu	Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg	
				405					410					415		
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr	
			420					425					430			
Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys	
		435					440					445				
Val	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val	
	450					455					460					
Trp	Val	Ala	Leu	Asn	Asn	Val	Lys	Ala	Ser	Thr	Asn	Ser	Pro	Trp	Glu	
465					470											

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<210> 39
<211> 1521
<212> DNA
<213> Artificial Sequence
<220>
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<223> 5' 519 bp from *A. thaliana* FAE1 (SEQ ID NO:1) and  
 3' 1002 bp from *B. napus* elongase KCS (SEQ ID  
 NO:3) and having a mutation at position 920;  
 designated At173 G307D

<221> CDS

<222> (1)...(1518)

<400> 39

atg	acg	tcc	ggt	aac	ggt	aag	ctc	ctt	tac	cgt	tac	gtc	tta	acc	aac	48
Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn	
1				5					10					15		

ttt	ttc	aac	ctc	tgt	ttg	ttc	ccg	tta	acg	gcg	ttc	ctc	gcc	gga	aaa	96
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys	
		20						25					30			

gcc	tct	cgg	ctt	acc	ata	aac	gat	ctc	cac	aac	ttc	ctt	tcc	tat	ctc	144
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu	
		35					40					45				

caa	cac	aac	ctt	ata	aca	gta	act	tta	ctc	ttt	gct	ttc	act	ggt	ttc	192
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe	
	50					55				60						

ggg	ttg	ggt	ctc	tac	atc	gta	acc	cga	ccc	aat	ccg	ggt	tat	ctc	ggt	240
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val	
65					70					75					80	

gac	tac	tcg	tgt	tac	ctt	cca	cca	ccg	cat	ctc	aaa	ggt	agt	gtc	tct	288
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Lys	Val	Ser	Val	Ser	
			85						90					95		

aaa	gtc	atg	gat	att	ttc	tac	caa	ata	aga	aaa	gct	gat	act	tct	tca	336
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser	
			100					105					110			

cgg	aac	gtg	gca	tgt	gat	gat	ccg	tcc	tcg	ctc	gat	ttc	ctg	agg	aag	384
Arg	Asn	Val	Ala	Cys	Asp	Asp	Pro	Ser	Ser	Leu	Asp	Phe	Leu	Arg	Lys	
		115					120					125				

att	caa	gag	cgt	tca	ggg	cta	ggg	gat	gag	acg	tac	agt	cct	gag	gga	432
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	Tyr	Ser	Pro	Glu	Gly	
	130					135					140					

ctc	att	cac	gta	cca	ccg	cgg	aag	act	ttt	gca	gcg	tca	cgt	gaa	gag	480
Leu	Ile	His	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ser	Arg	Glu	Glu	
145					150					155				160		

aca	gag	aag	ggt	atc	atc	ggg	gcg	ctc	gaa	aat	cta	ttc	aag	aac	acc	528
Thr	Glu	Lys	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr	
			165					170					175			

aac	ggt	aac	cct	aaa	gat	ata	ggg	ata	ctt	gtg	gtg	aac	tca	agc	atg	576
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	
			180				185					190				

ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys 195 200 205	624
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser 210 215 220	672
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His 225 230 235 240	720
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn 245 250 255	768
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe 260 265 270	816
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg 275 280 285	864
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly 290 295 300	912
gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn 305 310 315 320	960
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly 325 330 335	1008
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro 340 345 350	1056
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu 355 360 365	1104
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala 370 375 380	1152
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val 385 390 395 400	1200
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg 405 410 415	1248

tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat 1296  
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr  
                   420                                  425                                  430

gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa 1344  
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys  
                   435                                  440                                  445

gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt 1392  
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val  
                   450                                  455                                  460

tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa 1440  
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu  
 465                                  470                                  475                                  480

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag 1488  
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys  
                                   485                                  490                                  495

tca gag act cgt gtc caa aac ggt cgg tcc taa 1521  
 Ser Glu Thr Arg Val Gln Asn Gly Arg Ser  
                   500                                  505

<210> 40

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 173 amino acids from A. thaliana FAE1 (SEQ ID  
 NO:2) and 3' 333 amino acids from B. napus  
 elongase KCS (SEQ ID NO:4) having a mutation at  
 residue 307; designated At173 G307D; hypothetical

<400> 40

Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn  
 1                                  5                                  10                                  15  
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys  
                   20                                  25                                  30  
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu  
                   35                                  40                                  45  
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe  
                   50                                  55                                  60  
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val  
 65                                  70                                  75                                  80  
 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser  
                   85                                  90                                  95  
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser  
                   100                                  105                                  110  
 Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys  
                   115                                  120                                  125  
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly  
                   130                                  135                                  140

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Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu
145                               150                               155                               160
Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
                               165                               170                               175
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
                               180                               185                               190
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
                               195                               200                               205
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
                               210                               215                               220
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
225                               230                               235                               240
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
                               245                               250                               255
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
                               260                               265                               270
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
                               275                               280                               285
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
290                               295                               300
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
305                               310                               315                               320
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
                               325                               330                               335
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
                               340                               345                               350
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
                               355                               360                               365
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
370                               375                               380
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
385                               390                               395                               400
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
                               405                               410                               415
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
                               420                               425                               430
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
                               435                               440                               445
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
450                               455                               460
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
465                               470                               475                               480
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
                               485                               490                               495
Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
                               500                               505

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<210> 41

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 1197 bp from *B. napus* elongase KCS (SEQ ID NO:3) and 3' 324 bp from *A. thaliana* FAE1 (SEQ ID NO:1) and having a mutation at nucleotide position

920; designated Bn399 G307D; hypothetical

&lt;221&gt; CDS

&lt;222&gt; (1) ... (1518)

&lt;400&gt; 41

atg acg tcc att aac gtt aag ctc ctt tac cat tac gtc ata acc aac	48
Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn	
1 5 10 15	
ctt ttc aac ctt tgc ttc ttt ccg tta acg gcg atc gtc gcc gga aaa	96
Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys	
20 25 30	
gcc tat cgg ctt acc ata gac gat ctt cac cac tta tac tat tcc tat	144
Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr	
35 40 45	
ctc caa cac aac ctc ata acc atc gct cca ctc ttt gcc ttc acc gtt	192
Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val	
50 55 60	
ttc ggt tgc gtt ctc tac atc gca acc cgg ccc aaa ccg gtt tac ctc	240
Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu	
65 70 75 80	
gtt gag tac tca tgc tac ctt cca cca acg cat tgt aga tca agt atc	288
Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile	
85 90 95	
tcc aag gtc atg gat atc ttt tat caa gta aga aaa gct gat cct tct	336
Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser	
100 105 110	
cgg aac ggc acg tgc gat gac tcg tcg tgg ctt gac ttc ttg agg aag	384
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly	
130 135 140	
ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag	480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu	
145 150 155 160	
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc	528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	
165 170 175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg	576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	



195	200	205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser 210 215 220			672
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His 225 230 235 240			720
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn 245 250 255			768
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe 260 265 270			816
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg 275 280 285			864
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly 290 295 300			912
gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn 305 310 315 320			960
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly 325 330 335			1008
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro 340 345 350			1056
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu 355 360 365			1104
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala 370 375 380			1152
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg atc gat gag Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu 385 390 395 400			1200
cta gag aag aac tta gga cta tcg ccg atc gat gtg gag gca tct aga Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg 405 410 415			1248
tca acg tta cat aga ttt ggg aat act tca tct agc tca att tgg tat Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr			1296

420	425	430	
gaa tta gca tac ata gag gca aag gga aga atg aag aaa ggg aat aaa			1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys			
435	440	445	
gct tgg cag att gct tta gga tca ggg ttt aag tgt aat agt gcg gtt			1392
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val			
450	455	460	
tgg gtg gct cta cgc aat gtc aag gca tcg gca aat agt cct tgg caa			1440
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln			
465	470	475	480
cat tgc atc gat aga tat ccg gtt aaa att gat tct gat ttg tca aag			1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys			
485	490	495	
tca aag act cat gtc caa aac ggt cgg tcc taa			1521
Ser Lys Thr His Val Gln Asn Gly Arg Ser			
500	505		

<210> 42  
 <211> 506  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> 5' 399 amino acids from B. napus elongase KCS (SEQ  
 ID NO:3) and 3' 107 amino acids from A. thaliana  
 FAE1 (SEQ ID NO:1) having a mutation at residue  
 306; designated Bn399 G307D; hypothetical

<400> 42

Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn			
1	5	10	15
Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys			
20	25	30	
Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr			
35	40	45	
Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val			
50	55	60	
Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu			
65	70	75	80
Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile			
85	90	95	
Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser			
100	105	110	
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys			
115	120	125	
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly			
130	135	140	
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Arg Glu Glu			
145	150	155	160
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr			

				165						170						175	
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met		
			180					185					190				
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys		
		195					200					205					
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser		
	210					215					220						
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His		
225					230					235					240		
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn		
				245					250					255			
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe		
			260					265					270				
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg		
		275					280					285					
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly		
	290					295					300						
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn		
305					310					315					320		
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly		
				325					330					335			
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro		
			340					345					350				
Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu		
		355					360					365					
Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala		
	370					375					380						
Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Glu		
385					390					395					400		
Leu	Glu	Lys	Asn	Leu	Gly	Leu	Ser	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg		
			405						410					415			
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr		
			420					425					430				
Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys		
		435					440					445					
Ala	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val		
	450					455					460						
Trp	Val	Ala	Leu	Arg	Asn	Val	Lys	Ala	Ser	Ala	Asn	Ser	Pro	Trp	Gln		
465					470					475					480		
His	Cys	Ile	Asp	Arg	Tyr	Pro	Val	Lys	Ile	Asp	Ser	Asp	Leu	Ser	Lys		
				485					490					495			
Ser	Lys	Thr	His	Val	Gln	Asn	Gly	Arg	Ser								
			500					505				</					

<210> 43

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> primer for PCR

<400> 43

gcgctcga aa atctattcaa qaaca

<210> 44

<211> 33  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer for PCR  
  
 <400> 44  
 gttcttgaat agattttcga gcgcaccgat gat 33  
  
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 cggaacggca cgtgtgatga ttcgtcct 28  
  
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 aggacggatc atcacacgcg acgttccg 28  
  
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